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Database :
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Listing first 45 summaries
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Perfect score:
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SPTREMBL_15:*

1: sp_archea:*
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8: sp_organel:
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11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
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Gapop 10.0 , Gapext 0.5
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355
1 KRDPQQREYEDCRRRCEQQE.....MMNPQRGGSGRYEEGEEEQS 63
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                                                                                                               sp_invertebrate:*
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sp_bacteria:*
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sp_rodent:*
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 sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	U	4	ω	. 2	1	Result	
79	79	79	79	79.5	80.5	81.5	. 81.5	82	82	86	87	92	112	120	125.5	320	332	355	Score	
22.3	22.3	22.3	22.3	22.4	22.7	23.0	23.0	23.1	23.1	24.2	24.5	25.9	31.5	33.8	35.4	90.1	93.5	100.0	Query	фD
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Q9jm92 mus musculu	Q9p2r8 homo sapien	Q9w4j3 drosophila	P91419 caenorhabdi	O81254 zea mays su	Q9s709 arabidopsis	O81261 tripsacum d	O81260 tripsacum d		Q9vjj8 drosophila	Q24754 drosophila	Q9nua2 homo sapien	Q9zwi3 cucurbita m	Q03678 hordeum vul	Q43358 theobroma c	. Q9sew4 juglans reg	Q9spl3 macadamia i	Q9spl4 macadamia i	Q9spl5 macadamia i	Description	

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ALIGNMENTS

Qy 61 EQS 63 Db 246 EQS 248 RESULT 2	Qy 1 KRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQROHGRGGDMMNPQRGGSGRYEEGEE 60	Query Match 100.0%; Score 355; DB 10; Length 666; Best Local Similarity 100.0%; Pred. No. 4.7e-35; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps	AC OSSPLS; DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-CT-2000 (TrEMBLrel. 15, Last annotation update) DT 01-CT-2000 (TrEMBLrel. 15, Last annotation update) DE VICILIN PRECURSOR. GN Macadamia integrifolia (Macadamia nut). CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; CC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia. CC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia. CX NCBL_TaxID=60698; RN [1] RR SEQUENCE FROM N.A. RC TISSUE=NUT KERNEL; RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.; RA family of antimicrobial peptides is produced by processing of a 7 "A family of antimicrobial peptides is produced by processing of a 7 plant J. 0:0-0(1999). RR HSSP; PO0353; 2PHL. DR HSSP; PO0353; 2PHL. DR EMBL; AF161883; AAD54244.1; DR FFAM; PF00546; Seedstore_7s; 1. SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;	SULT 1
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SEQUENCE
                                                                                                                                       globulin protein in Macadamia integrifoi EMBL; AF161885; AAD54246
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EMBL; AF161884; AAD54245.1; -.

HSSP; P02853; 2PHL.
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Magnoliophyta; eudicotyledons; Proteaceae;
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043358; OTEMBLES C
01-NOV-1996 (TREMBLES C
01-NOV-1996 (TREMBLES C
01-OCT-2000 (TREMBLES C
"Comparison of the structure and nucleotide sequences of vicilin of coccoa and cotton raise questions about vicilin evolution."; plant Mol. Biol. 18:1173-1176(1992).
EMBL; x62625; CAA44493.1; -.
EMBL; x62626; CAA44494.1; -.
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Q9SEW4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                MEDLINE=92288309; PubMed=1600151; McHenry L., Fritz P.J.;
                                                                                                                              Theobroma cacao (Cacao).
Eukaryota; Viridiplantae; Embr:
Magnoliophyta; eudicotyledons;
Malvales; Malvaceae; Theobroma
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Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari
"Identification and cloning of a cDNA encoding a vicilin-like
Jug r 2, from English walnut kernel (Juglans regia): a major f
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   Q9ZWI3;
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"Barley embryo globulin 1 gene, Beg1: characterization chromosome mapping and regulation of expression.";
Mol. Gen. Genet. 239:209-218(1993).
EMRI. MA/177: NANAGORE
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Hordeum vulgare (Barley), a
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
PRODOM; PD081059; -; 1.
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01-OCT-2000
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INTERPRO; IPRO01113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02853; 2PHL.
MENDEL; 8553; Horvu;1188;8553.
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Heck G.R., Chamberlain A.C., Ho T
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INTERPRO; IPRO01113; -.
PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                         102 RHGEGEREE
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ENCE 637 AA; 72252 MW;
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T-2000 (TrEMBLrel.
STORAGE PROTEIN.
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24; Conser
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525 AA;
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01, Last sequence update)
15, Last annotation update)
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Embryophyta; Tracheophyta; Spermatophyta;
poales; Poaceae; Hordeum.
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Pred. No. 9.1e-07;
3; Mismatches 17;
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Pred. No. 1e-05;
B; Mismatches
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Q9NUA2;
01-OCT-2000
                                                                                                            Receptor.
NON_TER
SEQUENCE
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J. Biol. Chem. 274:2563-2570(1999).
EMBL; AB019195; BAA34056.1; -.
HYSERPRO; IPRO01113; -.
PPAM; PF00546; Seedstore_7s; 1.
PPODOM: PNDR1050...1
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ80804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cucurbita maxima (Pumpkin) (Winter squash).
Bukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; endicotyledons; core eudicots;
Cucurbitales; Cucurbitaceae; Cucurbita.
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58 QQQQQQQQQQQQQQQQQQQQTTSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ 115
                        5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ
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19; Conser
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                                                                                                              539 AA;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
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CAB87955.1;
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55444 MW;
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Pred. No. 0.00
15; Mismatches
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Pred. No. 0.0033;
Pred. No. 23;
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dicots; Rosidae; eurosids I;
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CG466B.
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01-NOV-1996
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                       MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Ceorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                 STRAIN-BERKELEY;
MEDLINE-7010
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila
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NCBI_TaxID=7244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94111143; PubMed=8283480;
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                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                               Neoptera;
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                                                                                                                                                                                                                                                                                                                                                             eoptera; Endopterygota; Diptera; Drosophilidae; Drosophila.
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E.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Helt G.,
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A Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reihert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syler E., Spradling A.C., Weinstock G.M., Weinsenbach J.,
A Syler E., Tanger T., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Kang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.
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Best Local :
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Q9VJJ9;
Q1-MAY-2000
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Hostin D., Ho
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                 MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle George R.A., Lewis S.E., Richards S., Ashburner M., Hendersc
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George R.A.,
Sutton G.G.,
                                                                                                                                                                                                                  Pterygota; Neoptera; Endoptephydroidea; Drosophilidae;
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PRINTS; PR00014; FNTYPEIII.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                       STRAIN-BERKELEY;
                                                                                                                                           SEQUENCE FROM N.A.
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Beeson K.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRLPQQHQGQAHQ----VAQQQQSQARNGNPQHPQRAGSSVGGASSVGTSEDGEDNSS
                                                                                                                                                                                                                                                                                                                                            PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                   melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                ) (TrEMBLrel. 13,
) (TrEMBLrel. 13,
) (TrEMBLrel. 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
  J.R.,
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                                                                                                                                                                                                                                          Endopterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An H.-J., Andrews-Pfannkoch C.,
  Yandell M.D.,
                                                                                                                                                                                                                  erygota; Diptera;
Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 82; DB
Pred. No. 0.08
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784AFD27DEE352F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1323
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Zhang
                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                             Brachycera; Muscomorpha;
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  0.
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  Chen
                        Henderson
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081260
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Best Local Similarity 36.2
        "Speciation and domestication in maize "speciation and domestication in maize evidence from the Globulin-1 gene."; Genetics 0:0-0(1998).
EMBL; AF064234; AAC31477.1; -.
                                                                                  Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; Liliopsida; Poales; Poac
NCBI_TaxID=4563;
                                                                                                                                        01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                GLOBULIN-1 (FRAGMENT).
                                                                                                                                                                  O81260;
01-NOV-1998
                                                                                                                                                                                         081260
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                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J. Harris N.D., Harris M.,
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0014; FNIYPEIII.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1
                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                                                                                          NTERPRO;
                                                                                                                                                                                                                                                                     14
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                                                                                                                                                                                                                                            RRLPQQHQGQAHQ----VAQQQQSQARNGNPQHPQRAGSSVGGASSVGTSEDGEDNSS
                                                                                                                                                                                                                                                                 RRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGS-----GRYEEGEEEQS
                                                                                                                                                                                                                                                                                                                                                                                 PF00041;
                                                                                                                                                                                                                                                                                                                                                                                          IPR001865;
                                                                                                                                                                                                                                                                                                                                               1323 AA;
                                                                                                                                                                                       PRELIMINARY;
1CAU
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                                                                                                                                                                                                                                                                                                                                                144904 MW;
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15,
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                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                937642564F61532D CRC64;
                                                                                               Poaceae;
                                                                                                                                                                                       242
                                          and
                                                                                                        Tracheophyta;
                                                                                                                                                                                                                                                                                                   0.082;
                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                      Ã
                                        its wild relatives:
                                                                                              Tripsacum
                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                             Length 1323;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                         Spermatophyta,
                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                             270
                                                                                                                                                                                                                                                                 63
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H.O.,
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O81261; PRELIMINARY; O81261; O1-NOV-1998 (Tremblrel 01-NOV-1998 (Tremblrel 01-CCT-2000 (Tremblrel 11-CCT-2000 (Tremblrel 11-CCT-2000)
                                                                                                                               Q9S709;
Q9S709;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                            T22C5.10.
T17H3.14.
             Chao Q., Brooks S., Buehler E., Shinn P., Altafi H., Bei Q., Ch
                                                                  Magnoliophyta; eudicotyledons;
Brassicales; Brassicaceae; Arab
                                                                                      Arabidopsis thaliana (Mous
Eukaryota; Viridiplantae;
                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       evidence from the Globulin-1 ger
Genetics 0.0-0(1998).
EMBL; AF064235; AAC31478.1; -.
HSSP; P50477; ICAU.
MENDEL; 31903; Trida;1188;31903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLOBULIN-1 (FRAGMENT).
Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta;
                                                        NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00546; Seedstore_7s; 1.
NON_TER 242 242
SEQUENCE 242 AA; 27810 MW;
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00867; CPSASE_2; UNKNOWN_1
NON_TER 246 246
                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO01113; -. PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnoliophyta; Liliopsida; Poales; NCBI_TaxID=4563;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilton H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Speciation and domestication in maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENDEL; 31902; Trida;1188;31902.
                                                                                                                                                                                                                                                                                                                                                                                [NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO01113;
                                                                                                                                                                                                                                                                        Local Similarity hes 19; Conser
                                                                                                                                                                                                                                38
                                                                                                                                                                                                                                                12 CRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQR---GGSGRYEEGEEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 CRRRCEQQEPRQQHQCOLRCREQQRQHGRGGDMMNPQR---GGSGRYEEGEEEQ
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                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                IPR000901;
                                                                                                                               ) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                            246 AA;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
    Α.,
                                                                                                                                                                                                                                                                                                                          28408 MW; 8D9B45991F9C5FB9 CRC64;
                                                                         (Mouse-ear cress).
ntae: Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27810 MW;
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35.2%;
                                                                                                                                13,
13,
    Hansen
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08,
                                                                 Arabidopsis
                                                                                                                                                                                                                                                                       8
E., Johnson-Hopson C., Kh
Chin C., Chiou J., Choi
en N., Howng B., Koo T.,
                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                      Score 81.5; I
Pred. No. 0.02
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.
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3; Mismatches
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Pred. No. 0
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Poaceae; Tripsacum.
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                                                                                                                                                                                                                                                                                 .02;
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                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                         Length 246;
                      Khan S., Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                     c.,
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RESULT 15
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DT 01-NOV
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                 Query Match
Best Local Similarity
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Best Local Similarity
 Matches
                                                                                        MENDEL; 31896; Zeana; 1188; 31896.

INTERPRO; IPRO00901; -.

INTERPRO; IPR001113; -.

PFAM; PF00546; Seedstore_7s; 1.

PROSITE; PS00867; CPSASE_2; UNKNOWN_1.

NON_TER 236 236

SEQUENCE 236 AA; 27050 MW; 36A7D94
                                                                                                                                                                                                                                                                                                                                                                                                                                                             O81254:
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO00504; -.
INTERPRO; IPRO00571; -.
PFAM; PF00076; rrm; 1.
PFAM; PF000642; zf-CCCH; 2.
SEQUENCE 296 AA; 34572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,
Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC T1/H3 sequence.";
"Arabidopsis thaliana chromosome 1 BAC T1/H3 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                 evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998)
EMBL; AF064222; AAC31465.1; -.
HSSP; P50477; ICAU
                                                                                                                                                                                                                                                                                                                                                                 2ea mays subsp. parviglumis.
Eukaryota; Viridiplantae; Embryophyta; Tracheoph
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TaxID=76912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       081254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AC012375; AAF24943.1; -. EMBL: AC005916; AAD46002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                           GLOBULIN-1 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                 Hilton H., Gaut B.S.;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               "Speciation and domestication in maize and its wild relatives:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 RRDPSHREFSHRDRDREFYRHGSGKRSSERSERQERDGSRGRRQASPKRGGSPGGGREGS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 EEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGS-GRYEEGE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EER 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                              236
27050 MW; 36A7D94C5213F206 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%;
                   22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana BAC T22C5 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.5; DB Pred. No. 0.032; 7; Mismatches
 8
Score 79.5; DB 10;
Pred. No. 0.034;
8; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F284D29BF68445BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
   Indels
                                    Length
                                        236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
   5
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   Gaps
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Search completed: March 1, 2001, 16:09:07 Job time: 1551 sec